

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Wiley, Steven R.
- (ii) TITLE OF THE INVENTION: MEMBER OF THE TNF FAMILY USEFUL FOR TREATMENT AND DIAGNOSIS OF DISEASE
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Abbott Laboratories, D377/AP6D
 - (B) STREET: 100 Abbott Park Road
 - (C) CITY: Abbott Park
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 60064
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/798692
 - (B) FILING DATE: 12-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Becker, Cheryl L.
 - (B) REGISTRATION NUMBER: 35,441
 - (C) REFERENCE/DOCKET NUMBER: 6048.US.P1
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 847-935-1729
 - (B) TELEFAX: 847-938-2623
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCCGCCC GTCGGAGCCA GAAGCGGAGG GGGCGCCGGG GGGAGCCGGG
 CACCGCCCTG 60
 CTGGTCCCGC TCGCGCTGGG CCTGGGCCTG GCGCTGGCCT GCCTCGGCCT
 CCTGCTGGCC 120
 GTGGTCAGTT TGGGGAGCCG GGCATCGCTG TCCGCCCAGG AGCCTGCCCA
 GGAGGAGCTG 180
 GTGGCAGAGG AGGACCAGGA CCCGTCGGAA CTGAATCCCC AGACAGAAGA
 AAGCCAGGAT 240
 CCTGCGCCTT TCCTGAACCG ACTAGTTCGG CCTCGAAGAA GTGCACCTAA
 AGGCCGAAA 300
 ACACGGGCTC GAAGAGCGAT CGCAGCCCAT TATGAAGTTC ATCCACGACC
 TGGACAGGAC 360
 GGAGCGCAGG CAGGTGTGGA CGGGACAGTG AGTGGCTGGG AGGAAGCCAG
 AATCAACAGC 420
 TCCAGCCCTC TGCCTACAA CCGCCAGATC GGGGAGTTTA TAGTCACCCG
 GGCTGGGCTC 480
 TACTACCTGT ACTGTCAGGT GCACTTTGAT GAGGGGAAGG CTGTCTACCT
 GAAGCTGGAC 540
 TTGCTGGTGG ATGGTGTGCT GGCCCTGCGC TGCCTGGAGG AATTCTCAGC
 CACTGCGGCG 600
 AGTTCCCTCG GGCCCCAGCT CCGCCTCTGC CAGGTGTCTG GGCTGTTGGC
 CCTGCGGCCA 660
 GGGTCCTCCC TGCAGATCCG CACCCTCCCC TGGGCCCATC TCAAGGCTGC
 CCCCTTCCTC 720
 ACCTACTTCG GACTCTTCCA GGTTCACCTGA GGGGCCCTGG TCTCCCCGCA
 GTCGTCCCAG 780
 GCTGCCGGCT CCCCTCGACA GCTCTCTGGG CACCCGGTCC CCTCTGCCCC
 ACCCTCAGCC 840
 GCTCTTTGCT CCAGACCTGC CCCTCCCTCT AGAGGCTGCC TGGGCCTGTT
 CACGTGTTTT 900
 CCATCCCACA TAAATACAGT ATTCCCCTC TTATCTTACA ACAACCCAC
 CGCCCACTCT 960
 CCACCTCACT AGCTCCCCAA TCCCTGACCC TTTGAGGCC CCAGTGATCT
 CGACTCCCCC 1020
 CTGGCCACAG ACCCCCAGGG CATTGTGTTC ACTGTACTCT GTGGGCAAGG
 ATGGGTCCAG 1080

AAGACCCAC TTCAGGCACT AAGAGGGGCT GGACCTGGCG GCAGGAAGCC
AAAGAGACTG 1140

GGCCTAGGCC AGGAGTTCCC AAATGTGAGG GGCGAGAAAC AAGACAAGCT
CCTCCCTTGA 1200

GAATTCCTG TGGATTTTGA AACAGATAT TATTTT
1236

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ala	Arg	Arg	Ser	Gln	Lys	Arg	Arg	Gly	Arg	Arg	Gly	Glu
Pro														
1				5				10					15	
Gly	Thr	Ala	Leu	Leu	Val	Pro	Leu	Ala	Leu	Gly	Leu	Gly	Leu	Ala
Leu														
			20					25					30	
Ala	Cys	Leu	Gly	Leu	Leu	Leu	Ala	Val	Val	Ser	Leu	Gly	Ser	Arg
Ala														
		35					40					45		
Ser	Leu	Ser	Ala	Gln	Glu	Pro	Ala	Gln	Glu	Glu	Leu	Val	Ala	Glu
Glu														
	50					55				60				
Asp	Gln	Asp	Pro	Ser	Glu	Leu	Asn	Pro	Gln	Thr	Glu	Glu	Ser	Gln
Asp														
65					70					75				
80														
Pro	Ala	Pro	Phe	Leu	Asn	Arg	Leu	Val	Arg	Pro	Arg	Arg	Ser	Ala
Pro														
			85					90					95	
Lys	Gly	Arg	Lys	Thr	Arg	Ala	Arg	Arg	Ala	Ile	Ala	Ala	His	Tyr
Glu														
			100					105					110	
Val	His	Pro	Arg	Pro	Gly	Gln	Asp	Gly	Ala	Gln	Ala	Gly	Val	Asp
Gly														
		115					120					125		
Thr	Val	Ser	Gly	Trp	Glu	Glu	Ala	Arg	Ile	Asn	Ser	Ser	Ser	Pro
Leu														
	130					135				140				
Arg	Tyr	Asn	Arg	Gln	Ile	Gly	Glu	Phe	Ile	Val	Thr	Arg	Ala	Gly
Leu														
145					150					155				
160														

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Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys Ala Val
 Tyr
 165 170 175
 Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu Arg Cys
 Leu
 180 185 190
 Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro Gln Leu
 Arg
 195 200 205
 Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly Ser Ser
 Leu
 210 215 220
 Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala Pro Phe
 Leu
 225 230 235
 240
 Thr Tyr Phe Gly Leu Phe Gln Val His
 245

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Val Met Met Leu Arg Thr Trp Arg Leu Leu Pro Met Val Leu
 Leu
 1 5 10 15
 Ala Ala Tyr Cys Tyr Cys Ser Leu Ala Ala Pro Gly Ser Asp Tyr
 Lys
 20 25 30
 Asp Asp Asp Asp Lys Gly Arg Lys Thr Arg Ala Arg Arg Gly Ile
 Ala
 35 40 45
 Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln
 Ala
 50 55 60
 Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn
 Ser
 65 70 75
 80
 Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val
 Thr
 85 90 95
 Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu
 Gly
 100 105 110
 Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu
 Ala

126

		115					120					125		
Leu	Arg	Cys	Leu	Glu	Glu	Phe	Ser	Ala	Thr	Ala	Ala	Ser	Ser	Leu
Gly														
	130					135				140				
Pro	Gln	Leu	Arg	Leu	Cys	Gln	Val	Ser	Gly	Leu	Leu	Ala	Leu	Arg
Pro														
145					150					155				
160														
Gly	Ser	Ser	Leu	Arg	Ile	Arg	Thr	Leu	Pro	Trp	Ala	His	Leu	Lys
Ala														
			165					170					175	
Ala	Pro	Phe	Leu	Thr	Tyr	Phe	Gly	Leu	Phe	Gln	Val	His		
			180					185						

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Lys	Trp	Val	Thr	Phe	Ile	Ser	Leu	Leu	Phe	Leu	Phe	Ser	Ser
Ala														
1			5					10					15	
Tyr	Ser	Arg	Gly	Val	Phe	Arg	Arg							
			20											

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
1				5			

0902106 021093

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Arg Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly
Gln
  1              5              10              15
Asp Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu
Glu
              20              25              30
Ala Arg Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile
Gly
              35              40              45
Glu Phe Ile Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln
Val
  50              55              60
His Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu
Val
  65              70              75
80
Asp Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr
Ala
              85              90              95
Ala Ser Ser Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly
Leu
              100              105              110
Leu Ala Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro
Trp
              115              120              125
Ala His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe
Gln
              130              135              140
Val His
145

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro
 Gln
 1 5 10 15
 Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
 Leu
 20 25 30
 Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
 Asn
 35 40 45
 Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
 His
 50 55 60
 Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
 Ile
 65 70 75
 80
 Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
 Thr
 85 90 95
 Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
 Tyr
 100 105 110
 Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
 Ser
 115 120 125
 Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
 Phe
 130 135 140
 Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
 His
 145 150 155
 160
 Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Ile
 Val
 165 170 175
 Gly

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Lys Gln Leu Ser Thr Pro Pro Leu Pro Arg Gly Gly Arg Pro
 Gln
 1 5 10 15
 Lys Val Ala Ala His Ile Thr Gly Ile Thr Arg Arg Ser Asn Ser
 Ala
 20 25 30

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[illegible]

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEO ID NO:9:

Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly
Gln														
1				5					10					15
Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly
Val														
			20					25					30	
Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr
Leu														
		35					40					45		
Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr
His														
	50					55					60			

130

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Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
Thr
65          70          75
80
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
Thr
          85          90          95
Pro Glu Gly Ala Glu Ala Lys Pro Trp Glu Pro Ile Tyr Leu Gly
Gly
          100          105          110
Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
Arg
          115          120          125
Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
Ile
          130          135          140
Ile Ala Ile
145

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Leu Lys Pro Ala Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn
Ser
1          5          10          15
Leu Leu Trp Arg Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly
Phe
          20          25          30
Ser Leu Ser Asn Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr
Phe
          35          40          45
Val Tyr Ser Gln Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys
Ala
          50          55          60
Thr Ser Ser Pro Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser
Ser
65          70          75
80
Gln Tyr Pro Phe His Val Pro Leu Leu Ser Ser Gln Lys Met Val
Tyr
          85          90          95
Pro Gly Leu Gln Glu Pro Trp Leu His Ser Met Tyr His Gly Ser
Ser
          100          105          110
Gly Gln Leu Thr Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly
Ile
          115          120          125

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Pro His Leu Val Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe
 Ala
 130 135 140
 Leu
 145

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile
 Asp
 1 5 10 15
 Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
 Leu
 20 25 30
 Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val
 Ala
 35 40 45
 Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg
 Val
 50 55 60
 Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
 Pro
 65 70 75
 80
 Gln Leu Arg Ser Ala Ala Gly Ala Ala Ile Ala Leu Thr Val Asp
 Leu
 85 90 95
 Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
 Gly
 100 105 110
 Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
 His
 115 120 125
 Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
 Thr
 130 135 140
 Val Leu Gly Leu Phe Arg Val Thr Pro Glu Leu Pro Ala Gly Leu
 Pro
 145 150 155
 160
 Ser Pro Arg Ser Glu
 165

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